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I hereby certify that the attached was transmitted via facsimile transmission to Assistant Commissioner for Patents, via facsimile number (703) 872-9307, on this 28th day of April, 2003.

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TO: Assistant Commissioner for Patents

FROM: Janice L. Rouse, Registration No. 52,183

RE: U. S. Patent Application No. 09/766,399; Attorney Docket No. 1165
Title: Novel Plant Promoters and Methods of Use

DATE: April 28, 2003 FAX NUMBER: (703) 872-9307

NUMBER OF PAGE(S) FOLLOWING THIS SHEET: 21

ATTENTION: Amendment/Response After Final Office Action

COMMENTS:

Attached –

- **Request for Reconsideration (1 copy)**
- **Petition for Extension of Time (2 copies)**

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Janice L. Rowe
AGENT/ATTORNEY FOR APPLICANT

4/28/2003
DATE

Attorney Docket No. 1165

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Bruce, et al.	Date:	April 28, 2003
Serial No.:	09/766,399	Group Art Unit:	1634
Filed:	January 19, 2001	Examiner:	Juliet C. Einsmann
For:	"Novel Plant Promoters and Methods of Use"		

Assistant Commissioner for Patents
Washington, D.C. 20231

REQUEST FOR RECONSIDERATION UNDER 37 CFR §1.116 TO FINAL OFFICE ACTION MAILED DECEMBER 26, 2002

STATUS OF CLAIMS

Claims 2-16 are in the application for consideration. Claims 1, 17 and 18 were cancelled without prejudice. No claims are allowed.

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AMENDMENTS

Status of amendments:

An amendment was submitted October 10, 2002. Following the entry of this Request for Reconsideration, Claims 2, 7, 8, 12, and 16 will have been amended and claims 1, 7, 17, and 18 will have been cancelled without prejudice.

Amendments to the claims:

Please cancel claim 7 without prejudice.

Amendments to claims 2, 8, and 12 are presented herewith. Examiner is requested to please amend the claims as follows:

2. (Amended) An isolated plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).

8. (Amended) A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

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(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).

12. (Amended) A plant cell having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to the nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).